SEQUENCE LISTING

<110> KAO CORPORATION

<120> Mutant alkali cellulase

<130> P

<150> JP P2002-124474

<151> 2002-04-25

<160> 6

<170> PatentIn Ver. 2.1

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<211> 824

<212> PRT

<213> Bacillus sp. KSM-S237

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Leu Val Leu Leu Leu Ser Leu Phe Pro Ala Ala Leu Ala Ala Glu Gly
            20                  25                  30

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
            35                  40                  45

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
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                50                      55                      60
Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly

     65                      70                      75                      80
Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn

                    85                      90                      95
Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu

                    100                     105                     110
Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile

                    115                     120                     125
Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met

                    130                     135                     140
Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp

     145                     150                     155                     160
Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu

                    165                     170                     175
Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser

                    180                     185                     190
Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp

                    195                     200                     205
Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys

     210                     215                     220
Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp

     225                     230                     235                     240
Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His

                    245                     250                     255
Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr

                    260                     265                     270
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21

Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met
          275   280   285

Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr
     290   295   300

Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro Tyr Phe Asp
305   310   315   320

Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp
               325   330   335

Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr
          340   345   350

Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp Pro Gly Pro
          355   360   365

Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val
     370   375   380

Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys
385   390   395   400

Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe
               405   410   415

Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala Val Asp Asn
          420   425   430

Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser Asn Asp Val
          435   440   445 ·

Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala Asn Gly Trp
     450   455   460

Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val
465   470   475   480

Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile Pro Gln Ser

22

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              485                490                495

Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg Val Asn Ala

          500                505                510

Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr

      515                520                525

Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala Phe His Glu

      530                535                540

Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly Thr Asp Ala

545                550                555                560

Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val

              565                570                575

Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser

          580                585                590

Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser

          595                600                605

Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala

      610                615                620

Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp

625        .        630                635                640

Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly

          645                650                655

Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala

              660                665                670

Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn

          675                680                685

Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu

      690                695                700


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Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys
705   710   715   720

Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg
                725   730   735

Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg
                740   745   750

Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro
                755   760   765

Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp
                770   775   780

Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys
785   790   795   800

Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala
                805   810   815

Val Lys Asn Glu Ala Lys Lys Lys
                820

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1   5   10   15

tta gtt tta ctt cta tct tta ttt ccg gca gct ctt gca gca gaa gga   96

Leu Val Leu Leu Leu Ser Leu Phe Pro Ala Ala Leu Ala Ala Glu Gly

            20   25   30

aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat gac aat gtt   144

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val

            35   40   45

aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc gat gga   192

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly

        50   55   60

caa atg aca tta gta gat caa cat gga gaa aaa att caa tta cgt gga   240

Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly

65   70   75   80

atg agt aca cac gga tta cag tgg ttt cct gag atc ttg aat gat aac   288

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn

            85   90   95

gca tac aaa gct ctt tct aac gat tgg gat tcc aat atg att cgt ctt   336

Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu

25

gct atg tat gta ggt gaa aat ggg tac gct aca aac cct gag tta atc   384

Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile

        115   120   125

aaa caa aga gtg att gat gga att gag tta gcg att gaa aat gac atg   432

Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met

        130   135   140

tat gtt att gtt gac tgg cat gtt cat gcg cca ggt gat cct aga gat   480

Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp

145   150   155   160

cct gtt tat gca ggt gct aaa gat ttc ttt aga gaa att gca gct tta   528

Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu

                165   170   175

tac cct aat aat cca cac att att tat gag tta gcg aat gag ccg agt   576

Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser

        180   185   190

agt aat aat aat ggt gga gca ggg att ccg aat aac gaa gaa ggt tgg   624

Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp

        195   200   205

aaa gcg gta aaa gaa tat gct gat cca att gta gaa atg tta cgt aaa   672

26

Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys
    210   215   220

agc ggt aat gca gat gac aac att atc att gtt ggt agt cca aac tgg   720
Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
225   230   235   240

agt cag cgt ccg gac tta gca gct gat aat cca att gat gat cac cat   768
Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
            245   250   255

aca atg tat act gtt cac ttc tac act ggt tca cat gct gct tca act   816
Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
            260   265   270

gaa agc tat ccg tct gaa act cct aac tct gaa aga gga aac gta atg   864
Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met
            275   280   285

agt aac act cgt tat gcg tta gaa aac gga gta gcg gta ttt gca aca   912
Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr
    290   295   300

gag tgg gga acg agt caa gct agt gga gac ggt ggt cct tac ttt gat   960
Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro Tyr Phe Asp
305   310   315   320

27

gaa gca gat gta tgg att gaa ttt tta aat gaa aac aac att agc tgg   1008
Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp
                325   330   335

gct aac tgg tct tta acg aat aaa aat gaa gta tct ggt gca ttt aca   1056
Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr
                340   345   350

cca ttc gag tta ggt aag tct aac gca acc aat ctt gac cca ggt cca   1104
Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp Pro Gly Pro
                355   360   365

gat cat gtg tgg gca cca gaa gaa tta agt ctt tct gga gaa tat gta   1152
Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val
                370   375   380

cgt gct cgt att aaa ggt gtg aac tat gag cca atc gac cgt aca aaa   1200
Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys
385   390   395   400

tac acg aaa gta ctt tgg gac ttt aat gat gga acg aag caa gga ttt   1248
Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe
                405   410   415

gga gtg aat tcg gat tct cca aat aaa gaa ctt att gca gtt gat aat   1296
Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala Val Asp Asn
                420   425   430

28

gaa aac aac act ttg aaa gtt tcg gga tta gat gta agt aac gat gtt   1344
Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser Asn Asp Val
       435   440   445

tca gat ggc aac ttc tgg gct aat gct cgt ctt tct gcc aac ggt tgg   1392
Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala Asn Gly Trp
       450   455   460

gga aaa agt gtt gat att tta ggt gct gag aag ctt aca atg gat gtt   1440
Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val
465   470   475   480

att gtt gat gaa cca acg acg gta gct att gcg gcg att cca caa agt   1488
Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile Pro Gln Ser
           485   490   495

agt aaa agt gga tgg gca aat cca gag cgt gct gtt cga gtg aac gcg   1536
Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg Val Asn Ala
          500   505   510

gaa gat ttt gtc cag caa acg gac ggt aag tat aaa gct gga tta aca   1584
Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr
          515   520   525

att aca gga gaa gat gct cct aac cta aaa aat atc gct ttt cat gaa   1632
Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala Phe His Glu

29

gaa gat aac aat atg aac aac atc att ctg ttc gtg gga act gat gca   1680
Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly Thr Asp Ala
545   550   555   560

gct gac gtt att tac tta gat aac att aaa gta att gga aca gaa gtt   1728
Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val
                         565   570   575

gaa att cca gtt gtt cat gat cca aaa gga gaa gct gtt ctt cct tct   1776
Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser
                    580   585   590

gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct gga gag tct   1824
Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser
                    595   600   605

ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt tct aac gcg   1872
Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala
               610   615   620

tta tca tgg gaa ttt gga tat cca gaa gta aaa cct agt gat aac tgg   1920
Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp
625   630   635   640

gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt   1968

30

Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly

           645   650   655

gag aat gat tat gta gct ttt gat ttc tat cta gat cca gtt cgt gca   2016

Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala

           660   665   670

aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac   2064

Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn

           675   680   685

ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa   2112

Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu

           690   695   700

tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa   2160

Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys

705   710   715   720

att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt   2208

Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg

           725   730   735

aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga   2256

Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg

           740   745   750

31

gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg   2304

Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro

          755   760   765

gtt gaa cca gag cca gtt gat cct ggc gaa gag acg cca cct gtc gat   2352

Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp

          770   775   780

gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa   2400

Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys

785   790   795   800

gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca   2448

Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala

             805   810   815

gtc aaa aat gag gct aag aaa aaa taa   2475

Val Lys Asn Glu Ala Lys Lys Lys

          820

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<212> DNA

<213> Artificial Sequence

<400> 4

ccattcgagt tagctcacgc aaatcttgac ccag 34

<210> 5

<211> 34

<212> DNA

<213> Artificial Sequence

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ccattcgagt tagctcgtgc aaatcttgac ccag 34

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<212> DNA

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caataacatc cattgtaagc ttctcagcac c 31